Hit List

Search Results - Record(s) 1 through 4 of 4 returned.

☐ 1. Document ID: WO 9915652 A1

Using default format because multiple data bases are involved.

```
L1: Entry 1 of 4                           File: EPAB              Apr 1, 1999


PUB-NO: WO009915652A1
DOCUMENT-IDENTIFIER: WO 9915652 A1
TITLE: MEGSIN PROTEIN

PUBN-DATE: April 1, 1999

INVENTOR-INFORMATION:
NAME                                        COUNTRY
MIYATA, TOSHIO                              JP

INT-CL (IPC): C12 N 15/12; C12 P 21/02; C12 N 1/21; C07 K 14/47; C07 K 16/18; G01 N
33/53; A01 K 67/027; C12 P 21/08
EUR-CL (EPC): C07K014/47
```

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw D |

☐ 2. Document ID: US 20040062274 A1, WO 200031996 A2, AU 200020123 A, BR
9915652 A, EP 1133886 A2, KR 2001080562 A, TW 444460 A, ZA 200103992 A, CN 1333981
A, MX 2001005147 A1, JP 2002531026 W, AU 766016 B, AU 2003231679 A1

```
L1: Entry 2 of 4                           File: DWPI              Apr 1, 2004


DERWENT-ACC-NO: 2000-542966
DERWENT-WEEK: 200425
COPYRIGHT 2005 DERWENT INFORMATION LTD
TITLE: Discontinuous data transmission method for mobile communication adaptive
multi rate system, involves transmitting silent descriptor frames between system
components based on detected period of source data inactivity

INVENTOR: BLOCHER, P; BRUHN, S ; HAKANSSON, S ; HELLWIG, K ; BLOECHER, P

PRIORITY-DATA: 1999US-0444368 (November 22, 1999), 1998US-109694P (November 24,
1998), 2003AU-0231679 (August 7, 2003), 2003US-0676342 (October 1, 2003)

PATENT-FAMILY:
```

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
US 20040062274 A1	April 1, 2004		000	H04J003/16

KR 2001030648 A, AU 200227633 A

L1: Entry 4 of 4   File: DWPI   Aug 20, 2002

DERWENT-ACC-NO: 1999-276983
DERWENT-WEEK: 200258
COPYRIGHT 2005 DERWENT INFORMATION LTD
TITLE: Megsin protein expressed specifically in mesangial cells

INVENTOR: MIYATA, T

PRIORITY-DATA: 1997JP-0275302 (September 22, 1997), 2002AU-0027633 (March 25, 2002)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
JP 2000512944 X	August 20, 2002		000	C12N015/09
WO 9915652 A1	April 1, 1999	J	100	C12N015/12
AU 9890963 A	April 12, 1999		000	
EP 1018551 A1	July 12, 2000	E	000	C12N015/12
KR 2001030648 A	April 16, 2001		000	C07K014/00
AU 200227633 A	May 16, 2002		000	A01K067/027

INT-CL (IPC): A01 K 67/027; C07 K 14/00; C07 K 14/47; C07 K 16/18; C12 N 1/21; C12 N 15/09; C12 N 15/12; C12 P 21/02; C12 P 21/08; G01 N 33/53

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw De |

Clear   Generate Collection   Print   Fwd Refs   Bkwd Refs

Generate OACS

Terms	Documents
9915652	4

Display Format: |-   Change Format

Previous Page   Next Page   Go to Doc#

WO 200031996 A2	June 2, 2000	E	056	H04Q007/30
AU 200020123 A	June 13, 2000		000	
BR 9915652 A	August 7, 2001		000	H04Q007/30
EP 1133886 A2	September 19, 2001	E	000	H04Q007/30
KR 2001080562 A	August 22, 2001		000	H04B014/04
TW 444460 A	July 1, 2001		000	H04L012/00
ZA 200103992 A	February 27, 2002		065	H04Q000/00
CN 1333981 A	January 30, 2002		000	H04Q007/30
MX 2001005147 A1	August 1, 2001		000	H04Q007/30
JP 2002531026 W	September 17, 2002		054	H04J003/00
AU 766016 B	October 9, 2003		000	H04Q007/30
AU 2003231679 A1	September 11, 2003		000	H04Q007/30

INT-CL (IPC): G10 L 11/02; G10 L 19/00; H04 B 14/04; H04 J 3/00; H04 J 3/16; H04 L 12/00; H04 Q 0/00; H04 Q 7/30

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw D |

☐ 3. Document ID: WO 9934639 A2, FI 9704532 A, AU 9915652 A, EP 1038241 A2, FI 109073 B1, US 6587899 B1

L1: Entry 3 of 4   File: DWPI   Jul 8, 1999

DERWENT-ACC-NO: 1999-405622
DERWENT-WEEK: 200347
COPYRIGHT 2005 DERWENT INFORMATION LTD
TITLE: Selective data transmission method for telecommunications system such as telephone exchange

INVENTOR: JAERVI, J; POIKOLAINEN, K ; JARVI, J

PRIORITY-DATA: 1997FI-0004532 (December 16, 1997)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
WO 9934639 A2	July 8, 1999	E	015	H04Q011/04
FI 9704532 A	June 17, 1999		000	H04Q000/00
AU 9915652 A	July 19, 1999		000	H04Q011/04
EP 1038241 A2	September 27, 2000	E	000	G06F017/30
FI 109073 B1	May 15, 2002		000	H04Q011/04
US 6587899 B1	July 1, 2003		000	G06F013/14

INT-CL (IPC): G06 F 13/14; G06 F 13/36; G06 F 13/364; G06 F 13/38; G06 F 17/30; H04 Q 0/00; H04 Q 3/545; H04 Q 11/04

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw D |

☐ 4. Document ID: JP 2000512944 X, WO 9915652 A1, AU 9890963 A, EP 1018551 A1,

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Search in Swiss-Prot and TrEMBL for: megsin

Swiss-Prot Release 45.5 of 04-Jan-2005
TrEMBL Release 28.5 of 04-Jan-2005

- Number of sequences found in <u>Swiss-Prot</u>$_{(2)}$ and <u>TrEMBL</u>$_{(1)}$: **3**
- Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the <u>bottom</u> of this page.
- For more directed searches, you can use the Sequence Retrieval System <u>SRS</u>.

Search in Swiss-Prot: There are matches to 2 out of 167089 entries

<u>SPB7_HUMAN</u> **(O75635)**
    Megsin (TP55) (Serpin B7). {GENE: Name=SERPINB7} - Homo sapiens (Human)
<u>SPB7_MOUSE</u> **(Q9D695)**
    Megsin (Serpin B7). {GENE: Name=Serpinb7} - Mus musculus (Mouse)

Search in TrEMBL: There are matches to 1 out of 1560235 entries

<u>Q920J5</u>
    Megsin {GENE:Name=Serpinb7} - Rattus norvegicus (Rat)

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NиceProt View of TrEMBL: Q6P3F8

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[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**Q6P3F8**
Primary accession number	**Q6P3F8**
Secondary accession numbers	None
Entered in TrEMBL in	Release 27, July 2004
Sequence was last modified in	Release 27, July 2004
Annotations were last modified in	Release 27, July 2004

Name and origin of the protein

Protein name	**Serine (Or cysteine) proteinase inhibitor, clade B, member 7**
Synonyms	None
Gene name	**Name: Serpinb7**
From	Mus musculus (Mouse) [TaxID: 10090]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

References

[1] NUCLEOTIDE SEQUENCE.
   TISSUE=Jaw and Limb;
   DOI=10.1073/pnas.242603899;MEDLINE=22388257;PubMed=12477932 [NCBI, ExPASy, EBI, Israel, Japan]
   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., ▦▦ , Marra M.A.;
   "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2] NUCLEOTIDE SEQUENCE.
   TISSUE=Jaw and Limb;
   Strausberg R.;
   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

Comments

- *FUNCTION*: Component of the nuclear pore complex, a complex required for the trafficking

across the nuclear membrane *(By similarity)*.
- *SUBCELLULAR LOCATION*: Central region of the nuclear pore complex, within the transporter. Localizes on both cytoplasmic and nucleoplasmic sides of the nuclear pore complex near the central gated channel *(By similarity)*.
- *DOMAIN*: Contains FG repeats *(By similarity)*.
- *SIMILARITY*: Belongs to the serpin family.

Cross-references

EMBL	BC064004; AAH64004.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
HSSP	P05121; 1A7C. [HSSP ENTRY / PDB]
GO	GO:0004867; Molecular function: serine-type endopeptidase inhibitor activity *(inferred from electronic annotation)*. QuickGo view.
InterPro	IPR000215; Prot_inh_serpin. Graphical view of domain structure.
Pfam	PF00079; Serpin; 1. Pfam graphical view of domain structure.
SMART	SM00093; SERPIN; 1.
PROSITE	PS00284; SERPIN; UNKNOWN_1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOVERGEN	[Family / Alignment / Tree]
ProtoMap	Q6P3F8.
PRESAGE	Q6P3F8.
ModBase	Q6P3F8.
SMR	Q6P3F8; 3C240272A9FB935E.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Coiled coil; **Nuclear protein**; **Protease inhibitor**; **Repeat**; **Serine protease inhibitor**; **Serpin**; **Transport**.

Features

None

Sequence information

Length: **380 AA**   Molecular weight: **43020 Da**   CRC64: **3C240272A9FB935E** [This is a checksum on the sequence]

```
        10         20         30         40         50         60
MASLAAANAE FGFDLFREMD SSQGNGNVFF SSLSIFTALT LIRLGARGDC ARQIDKALHF

        70         80         90        100        110        120
NIPSRQGNSS NNQPGLQYQL KRVLADINSS HKDYELSIAT GVFAEKVYDF HKNYIECAEN

       130        140        150        160        170        180
LYNAKVERVD FTNDVQDTRF KINKWIENET HGKIKKVLGD SSLSSSAVMV LVNAVYFKGK

       190        200        210        220        230        240
WKSAFTKTDT LSCRFRSPTC PGKVVNMMHQ ERRFNLSTIQ QPPMQVLELQ YHGGISMYIM
```

```
        250 '     260         270         280         290         300
LPEDGLCEIE SKLSFQNLMD WANRRKMKSQ YVNVFLPQFK IEKNYEMTHH LKSLGLKDIF

        310         320         330         340         350         360
DESSADLSGI ASGGRLYVSK LMHKSFIEVS EEGTEATAAT ENNIVEKQLP ESTVFRADRP

        370         380
FLFVIKKNDI ILFTGKVSCP
```

Q6P3F8 in FASTA format

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BLAST BLAST submission on ExPASy/SIB or at NCBI (USA)

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ScanProsite, MotifScan

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```
==========================================================================

                   Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that
the computation was performed at the SIB using the BLAST network service.
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BLAST 2 software.

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If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W.,
Lipman D.J.  Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs.  Nucleic Acids Res. 25:3389-3402(1997).


==========================================================================


Query:  15 AA
Date run: 2005-01-27 10:03:50 UTC+0100 on sib-gml.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
           1,737,387 sequences; 556,730,939 total letters
UniProt Release 3.5 consists of: Swiss-Prot Release 45.5 of 04-Jan-2005:   167089 en
                                 TrEMBL Release 28.5 of 04-Jan-2005:  1560235 entrie
```

[Taxonomic view]   [NiceBlast view]   [Printable view]

List of potentially matching sequences
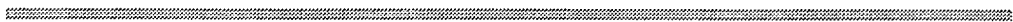
Send selected sequences to [Clustal W (multiple alignment) ▼] [Submit Query]

[Select up to...]
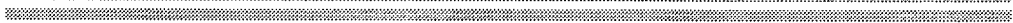
☐ Include query sequence

```
   Db AC        Description                                              Score E-value

☐ sp O75635 SPB7_HUMAN Megsin (TP55) (Serpin B7) [SERPINB7] [Homo ...   55 2e-07
☐ sp Q9D695 SPB7_MOUSE Megsin (Serpin B7) [Serpinb7] [Mus musculus...  46 7e-05
☐ tr Q920J5 Megsin [Serpinb7] [Rattus norvegicus (Rat)]               46 7e-05
☐ tr Q6P3F8 Serine (Or cysteine) proteinase inhibitor, clade B, me... 46 7e-05
```

Graphical overview of the alignments

[Click here] to resubmit your query after masking regions matching PROSITE profiles
or Pfam HMMs

(Help) (use ScanProsite for more details about PROSITE matches)

```
Profile hits   ░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░
Pfam hits      ░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░

               Matches on query sequence                                Mat
Submission     ████████████████████████████████████████████████████████ ██
               1                                                          1

SPB7_HUMAN     ░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░ ░░
SPB7_MOUSE     ░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░ ░░
Q920J5         ░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░ ░░
Q6P3F8         ░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░ ░░

               1
Submission     ████████████████████████████████████████████████████████
               ▓▓▓▓▒▒▒▒▒░░░░░░░

Identity       0     25    50    75    100%
```

Alignments

sp O75635   **Megsin (TP55) (Serpin B7) [SERPINB7] [Homo sapiens   380**
   SPB7_HUMAN **(Human)]**   AA
                                                                         align

 Score = 54.5 bits (121), Expect = 2e-07
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1   FREMDDNQGNGNVFF 15
            FREMDDNQGNGNVFF
Sbjct: 16   FREMDDNQGNGNVFF 30

sp Q9D695   **Megsin (Serpin B7) [Serpinb7] [Mus musculus (Mouse)]** 380 AA
   SPB7_MOUSE

                                                                      align

 Score = 46.0 bits (101), Expect = 7e-05
 Identities = 13/15 (86%), Positives = 13/15 (86%)

Query: 1   FREMDDNQGNGNVFF 15
            FREMD QGNGNVFF
Sbjct: 16   FREMDSSQGNGNVFF 30

tr Q920J5 **Megsin [Serpinb7] [Rattus norvegicus (Rat)]** 380 AA

                                                                align

 Score = 46.0 bits (101), Expect = 7e-05
 Identities = 13/15 (86%), Positives = 13/15 (86%)

Query: 1   FREMDDNQGNGNVFF 15

```
               FREMD   QGNGNVFF
Sbjct: 16 FREMDSSQGNGNVFF 30
```

tr <u>Q6P3F8</u> **Serine (Or cysteine) proteinase inhibitor, clade B, member 7** 380 AA
                [Serpinb7] [Mus musculus (Mouse)]
                                                                          <u>align</u>

Score = 46.0 bits (101), Expect = 7e-05
Identities = 13/15 (86%), Positives = 13/15 (86%)

```
Query: 1   FREMDDNQGNGNVFF 15
              FREMD   QGNGNVFF
Sbjct: 16 FREMDSSQGNGNVFF 30
```

Database: EXPASY/UniProt
    Posted date: Jan 3, 2005 6:58 PM
  Number of letters in database: 556,730,939
  Number of sequences in database: 1,737,387

Lambda   K   H
   0.333   0.281   1.80

Gapped
Lambda   K   H
   0.294   0.110   0.610

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of HSP's successfully gapped in prelim test: 0
length of query: 15
length of database: 556,730,939
effective HSP length: 6
effective length of query: 9
effective length of database: 546,306,617
effective search space: 4916759553
effective search space used: 4916759553
T: 16
A: 40
X1: 15 (7.2 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 41 (21.6 bits)
S2: 61 (29.1 bits)

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Entry information

Entry name	**Q920J5**
Primary accession number	**Q920J5**
Secondary accession numbers	None
Entered in TrEMBL in	Release 19, December 2001
Sequence was last modified in	Release 19, December 2001
Annotations were last modified in	Release 26, March 2004

Name and origin of the protein

Protein name	**Megsin**
Synonyms	None
Gene name	**Name: Serpinb7**
From	Rattus norvegicus (Rat) [TaxID: 10116]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

References

[1] NUCLEOTIDE SEQUENCE.
   MEDLINE=21368006;PubMed=11473647 [NCBI, ExPASy, EBI, Israel, Japan]
   Nangaku M., Miyata T., Suzuki D., Umezono T., Hashimoto T., Wada T., Yagi M., Nagano N., Inagi R., Kurokawa K.;
   "Cloning of rodent megsin revealed its up-regulation in mesangioproliferative nephritis.";
   Kidney Int. 60:641-652(2001).

Comments

- *FUNCTION*: Component of the nuclear pore complex, a complex required for the trafficking across the nuclear membrane *(By similarity)*.
- *SUBCELLULAR LOCATION*: Central region of the nuclear pore complex, within the transporter. Localizes on both cytoplasmic and nucleoplasmic sides of the nuclear pore complex near the central gated channel *(By similarity)*.
- *DOMAIN*: Contains FG repeats *(By similarity)*.
- *SIMILARITY*: Belongs to the serpin family.

Cross-references

EMBL	AF105329; AAL16769.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
HSSP	P05121; 1A7C. [HSSP ENTRY / PDB]
Ensembl	ENSRNOG00000002555; Rattus norvegicus. [Contig view]
RGD	71063; Serpinb7.
GeneLynx	Serpinb7; Rattus norvegicus.
GO	GO:0004867; Molecular function: serine-type endopeptidase inhibitor activity *(inferred from electronic annotation).* QuickGo view.
InterPro	IPR000215; Prot_inh_serpin. Graphical view of domain structure.
Pfam	PF00079; Serpin; 1. Pfam graphical view of domain structure.
SMART	SM00093; SERPIN; 1.
PROSITE	PS00284; SERPIN; UNKNOWN_1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOVERGEN	[Family / Alignment / Tree]
ProtoMap	Q920J5.
PRESAGE	Q920J5.
ModBase	Q920J5.
SMR	Q920J5; D8076CA8EE2C2FBC.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Coiled coil; Nuclear protein; Protease inhibitor; Repeat; Serine protease inhibitor; Serpin; Transport.

Features

None

Sequence information

Length: **380 AA**   Molecular weight: **42820 Da**   CRC64: **D8076CA8EE2C2FBC** [This is a checksum on the sequence]

```
          10         20         30         40         50         60
MASLAAANAE FGFDLFREMD SSQGNGNVFF SSLSIFTALS LIRLGARGDC ARQIDKALHF

          70         80         90        100        110        120
ISPSRQGNSS NSQLGLQYQL KRVLADINSS HKDYELSIAN GVFAEKVFDF HKSYMECAEN

         130        140        150        160        170        180
LYNAKVERVD FTNDIQETRF KINKWIENET HGKIKKVLGD SSLSSSAVMV LVNAVYFKGK

         190        200        210        220        230        240
WKSAFTKSDT LSCHFRSPSG PGKAVNMMHQ ERRFNLSTIQ EPPMQILELQ YHGGISMYIM

         250        260        270        280        290        300
LPEDDLSEIE SKLSFQNLMD WTNSRKMKSQ YVNVFLPQFK IEKDYEMRSH LKSVGLEDIF

         310        320        330        340        350        360
VESRADLSGI ASGGRLYVSK LMHKSLIEVS EEGTEATAAT ESNIVEKLLP ESTVFRADRP
```

```
        370          380
FLFVIRKNGI ILFTGKVSCP
```

Q920J5 in FASTA
format

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or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)

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[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**SPB7_MOUSE**
Primary accession number	**Q9D695**
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 42, October 2003
Sequence was last modified in	Release 42, October 2003
Annotations were last modified in	Release 44, July 2004

Name and origin of the protein

Protein name	**Megsin**
Synonym	**Serpin B7**
Gene name	**Name: Serpinb7**
From	Mus musculus (Mouse) [TaxID: 10090]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

References

[1] NUCLEOTIDE SEQUENCE.
   DOI=10.1046/j.1523-1755.2001.060002641.x;MEDLINE=21368006;PubMed=11473647 [NCBI, ExPASy, EBI, Israel, Japan]
   Nangaku M., Miyata T., Suzuki D., Umezono T., Hashimoto T., Wada T., Yagi M., Nagano N., Inagi R., Kurokawa K.;
   "Cloning of rodent megsin revealed its up-regulation in mesangioproliferative nephritis.";
   Kidney Int. 60:641-652(2001).

[2] NUCLEOTIDE SEQUENCE.
   STRAIN=C57BL/6J;
   TISSUE=Skin;
   DOI=10.1038/nature01266;MEDLINE=22354683;PubMed=12466851 [NCBI, ExPASy, EBI, Israel, Japan]
   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach

C., Gojobori T., Baldarelli R., ▦ , Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).

Comments

- *FUNCTION*: Might function as an inhibitor of Lys-specific proteases. Might influence the maturation of megakaryocytes via its action as a serpin *(By similarity)*.
- *SUBCELLULAR LOCATION*: Cytoplasmic *(By similarity)*.
- *SIMILARITY*: Belongs to the serpin family. Ov-serpin subfamily.

Copyright

Cross-references

EMBL	AF105328; AAL16768.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AK014524; BAB29410.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
HSSP	P05121; 1A7C. [HSSP ENTRY / PDB]
MGD	MGI:2151053; Serpinb7.
CleanEx	MGI:2151053; Serpinb7.
GeneLynx	Serpinb7; Mus musculus.
SOURCE	Serpinb7; Mus musculus.
InterPro	IPR000215; Prot_inh_serpin.
	Graphical view of domain structure.
Pfam	PF00079; Serpin; 1.
	Pfam graphical view of domain structure.
SMART	SM00093; SERPIN; 1.
PROSITE	PS00284; SERPIN; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOVERGEN	[Family / Alignment / Tree]
BLOCKS	Q9D695.
ProtoNet	Q9D695.
ProtoMap	Q9D695.
PRESAGE	Q9D695.
DIP	Q9D695.
ModBase	Q9D695.
SMR	Q9D695; C9240272BCFB9CF4.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Serine protease inhibitor; Serpin.

Features
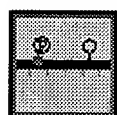
Feature table viewer

```
Key      From   To  Length   Description
SITE     347    348     2     Reactive bond (By similarity).
```

Sequence information

Length: **380 AA**   Molecular weight: **43050 Da**   CRC64: **C9240272BCFB9CF4** [This is a checksum on the sequence]

```
         10         20         30         40         50         60
MASLAAANAE FGFDLFREMD SSQGNGNVFF SSLSIFTALT LIRLGARGDC ARQIDKALHF

         70         80         90        100        110        120
NIPSRQGNSS NNQPGLQYQL KRVLADINSS HKDYELSIAT GVFAEKVYDF HKNYIECAEN

        130        140        150        160        170        180
LYNAKVERVD FTNDVQDTRF KINKWIENET HGKIKKVLGD SSLSSSAVMV LVNAVYFKGK

        190        200        210        220        230        240
WKSAFTKTDT LSCRFRSPTC PGKVVNMMHQ ERRFNLSTIQ QPPMQVLELQ YHGGISMYIM

        250        260        270        280        290        300
LPEDGLCEIE SKLSFQNLMD WTNRRKMKSQ YVNVFLPQFK IEKNYEMTHH LKSLGLKDIF

        310        320        330        340        350        360
DESSADLSGI ASGGRLYVSK LMHKSFIEVS EEGTEATAAT ENNIVEKQLP ESTVFRADRP

        370        380
FLFVIKKNDI ILFTGKVSCP
```

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BLAST   BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

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```
===========================================================================

                    Welcome to the SIB BLAST Network Service

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the computation was performed at the SIB using the BLAST network service.
The SIB BLAST network service uses a server developed at SIB and the NCBI
BLAST 2 software.

In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W.,
Lipman D.J.  Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs.  Nucleic Acids Res. 25:3389-3402(1997).


===========================================================================

Query:  15 AA
Date run: 2005-01-27 10:09:32 UTC+0100 on sib-gml.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
          1,737,387 sequences; 556,730,939 total letters
UniProt Release 3.5 consists of: Swiss-Prot Release 45.5 of 04-Jan-2005:    167089 en
                                 TrEMBL Release 28.5 of 04-Jan-2005:  1560235 entrie
```

[Taxonomic view]   [NiceBlast view]   [Printable view]

List of potentially matching sequences

Send selected sequences to `Clustal W (multiple alignment)` ▼   [Submit Query]
[Select up to...]

☐ Include query sequence


```
    Db AC      Description                                              Score E-value

☐ sp O75635 SPB7_HUMAN Megsin (TP55) (Serpin B7) [SERPINB7] [Homo ... 49 1e-05
☐ sp Q9D695 SPB7_MOUSE Megsin (Serpin B7) [Serpinb7] [Mus musculus... 29  6.6
☐ tr Q920J5 Megsin [Serpinb7] [Rattus norvegicus (Rat)]               29  6.6
☐ tr Q6P3F8 Serine (Or cysteine) proteinase inhibitor, clade B, me... 29  6.6
```

Graphical overview of the alignments

[Click here] to resubmit your query after masking regions matching PROSITE profiles
or Pfam HMMs

(🕮 Help) (use ScanProsite for more details about PROSITE matches)

```
Profile hits   ░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░
Pfam hits      ░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░

               Matches on query sequence                            Mat
Submission     ▌███████████████████████████████▐           ▎        ▬▬
               1                                                     1

SPB7_HUMAN     ░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░       ░░░
SPB7_MOUSE         ░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░       ░░░
Q920J5         ░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░       ░░░
Q6P3F8             ░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░░       ░░░

               1
Submission     ▌█████████████████████████████████████████▐  ▎
               ░░░░░░░░░░░░░░░░░░░░░░░░

Identity       0     25    50    75    100%
```

Alignments

sp <u>O75635</u>   **Megsin (TP55) (Serpin B7) [SERPINB7] [Homo sapiens**   380
   SPB7_HUMAN   **(Human)]**   AA
                                                                        <u>align</u>

 Score = 48.6 bits (107), Expect = 1e-05
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 SQSGLQSQLKRVFSD 15
           SQSGLQSQLKRVFSD
Sbjct: 72 SQSGLQSQLKRVFSD 86

sp <u>Q9D695</u>   **Megsin (Serpin B7) [Serpinb7] [Mus musculus (Mouse)]** 380 AA
   SPB7_MOUSE
                                                                  <u>align</u>

 Score = 29.5 bits (62), Expect = 6.6
 Identities = 10/14 (71%), Positives = 10/14 (71%)

Query: 2 QSGLQSQLKRVFSD 15
           Q GLQ QLKRV D
Sbjct: 73 QPGLQYQLKRVLAD 86

tr <u>Q920J5</u> **Megsin [Serpinb7] [Rattus norvegicus (Rat)]** 380 AA

                                                           <u>align</u>

 Score = 29.5 bits (62), Expect = 6.6
 Identities = 11/15 (73%), Positives = 11/15 (73%)

Query: 1 SQSGLQSQLKRVFSD 15

```
              SQ GLQ QLKRV  D
Sbjct: 72 SQLGLQYQLKRVLAD 86
```

tr Q6P3F8 **Serine (Or cysteine) proteinase inhibitor, clade B, member 7** 380 AA
          [Serpinb7] [Mus musculus (Mouse)]

                                                                    align

Score = 29.5 bits (62), Expect = 6.6
Identities = 10/14 (71%), Positives = 10/14 (71%)

```
Query: 2   QSGLQSQLKRVFSD 15
           Q GLQ QLKRV  D
Sbjct: 73  QPGLQYQLKRVLAD 86
```

Database: EXPASY/UniProt
    Posted date: Jan 3, 2005 6:58 PM
  Number of letters in database: 556,730,939
  Number of sequences in database: 1,737,387

```
Lambda     K       H
   0.347    0.287    1.65
```

Gapped
```
Lambda     K       H
   0.294    0.110    0.610
```

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of HSP's successfully gapped in prelim test: 0
length of query: 15
length of database: 556,730,939
effective HSP length: 6
effective length of query: 9
effective length of database: 546,306,617
effective search space: 4916759553
effective search space used: 4916759553
T: 16
A: 40
X1: 14 (7.0 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 40 (21.8 bits)
S2: 61 (29.1 bits)

Wallclock time: 127 seconds
```

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